SEQUENCE LISTING

<110> Nisson, Paul
    Jesse, Joel
    Li, Wu-bo

<120> Method for Isolating and Recovering Target DNA or RNA Molecules Having
    a Desired Nucleotide Sequence

<130> 0942.4800002

<141> 2001-04-10

<150> US 09/103,577
<151> 1998-06-24

<160> 11

<170> PatentIn version 3.0

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<223> consensus sequence for initiation of translation
        by eukaryotic ribosomes

<400> 11
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SEQUENCE LISTING

5

(1) GENERAL INFORMATION

(i) APPLICANT: Nisson, Paul
      Jessee, Joel
      Li, Wu-bo

10

(ii) TITLE OF THE INVENTION: Method of Nucleic Acid Sequence
    Selection

(iii) NUMBER OF SEQUENCES: 11

15

(iv) CORRESPONDENCE ADDRESS:
  (A) ADDRESSEE: Howrey & Simon
  (B) STREET: 1299 Pennsylvania Avenue, N.W.
  (C) CITY: Washington
  (D) STATE: DC

20
  (E) COUNTRY: USA
  (F) ZIP: 20004-2402

(v) COMPUTER READABLE FORM:
  (A) MEDIUM TYPE: Diskette

25
  (B) COMPUTER: IBM Compatible
  (C) OPERATING SYSTEM: DOS
  (D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

30
  (A) APPLICATION NUMBER:
  (B) FILING DATE:
  (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

35
  (A) APPLICATION NUMBER:
  (B) FILING DATE:

40

(viii) ATTORNEY/AGENT INFORMATION:
  (A) NAME: Auerbach, Jeffrey I
  (B) REGISTRATION NUMBER: 32,680
  (C) REFERENCE/DOCKET NUMBER: 04227.0026

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(ix) TELECOMMUNICATION INFORMATION:
  (A) TELEPHONE: 202 383-7451
  (B) TELEFAX: 202 383-6610
  (C) TELEX:

10

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 23 base pairs
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTNTGYGAYG GNTTYCAYGT NGG   23

25   (2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 19 base pairs
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: single
30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
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GTKTGGAGGK TTCAGTKGG   19

(2) INFORMATION FOR SEQ ID NO:3:

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GTKTGGAGGK TTCAGTGG   18

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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
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(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

20   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GTKTGGAGGT TCAGTKGG   18

(2) INFORMATION FOR SEQ ID NO:5:
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(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
30   (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

35   GTTGGAGGKT TCAGTKGG   18

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
40   (A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GTTGGAGGKT TCAGTGG   17

10   (2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
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(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

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GTKTGGAGGT TCAGTGG   17

(2) INFORMATION FOR SEQ ID NO:8:

25   (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTTGGAGGTT CAGTKGG   17
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(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
40   (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GTTGGAGGTT CAGTGG   16

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 25 base pairs
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GACCGTTCAG CTGGATATTA CGGCC   25

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 14 base pairs
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GCCGCCAGCC AUGG   14